SEQUENCE LISTING

<110> Shimkets, Richard
Carpenter, Thomas

<120> METHODS FOR DIAGNOSING AND TREATMENT OF CONDITIONS THAT ALTER PHOSPHATE TRANSPORT IN MAMMALS

<130> 21402-604

<140> Not yet assigned
<141> 2003-08-20

<150> 60/404,659
<151> 2002-08-20

<150> 60/463,219
<151> 2003-04-16

<160> 6

<170> CuraSeqList version 0.1

<210> 1
<211> 606
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (17)..(592)

<400> 1

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caccagatct cccacc atg cac aaa tgg ata ctg aca tgg atc ctg cca act  52
                  Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr
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ttg ctc tac aga tca tgc ttt cac att atc tgt cta gtg ggt act ata   100
Leu Leu Tyr Arg Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile
         15                  20                  25

tct tta gct tgc aat gac atg act cca gag caa atg gct aca aat gtg   148
Ser Leu Ala Cys Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val
     30                  35                  40

aac tgt tcc agc cct gag cga cac aca aga agt tat gat tac atg gaa   196
Asn Cys Ser Ser Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu
 45                  50                  55                  60

gga ggg gat ata aga gtg aga aga ctc ttc tgt cga aca cag tgg tac   244
Gly Gly Asp Ile Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr
                 65                  70                  75

ctg agg atc gat aaa aga ggc aaa gta aaa ggg acc caa gag atg aag   292
Leu Arg Ile Asp Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys
             80                  85                  90
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aat aat tac aat atc atg gaa atc agg aca gtg gca gtt gga att gtg   340
Asn Asn Tyr Asn Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val
         95                  100                 105

gca atc aaa ggg gtg gaa agt gaa ttc tat ctt gca atg aac aag gaa   388
Ala Ile Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu
    110                 115                 120

gga aaa ctc tat gca aag aaa gaa tgc aat gaa gat tgt aac ttc aaa   436
Gly Lys Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys
125                 130                 135                 140

gaa cta att ctg gaa aac cat tac aac aca tat gca tca gct aaa tgg   484
Glu Leu Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp
                145                 150                 155

aca cac aac gga ggg gaa atg ttt gtt gcc tta aat caa aag ggg att   532
Thr His Asn Gly Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile
            160                 165                 170

cct gta aga gga aaa aaa cga aga aag aac aaa aaa cag ccc act ttc   580
Pro Val Arg Gly Lys Lys Arg Arg Lys Asn Lys Lys Gln Pro Thr Phe
        175                 180                 185

ttc cta tgg caa taactgtcga cggc                                  606
Phe Leu Trp Gln
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<211> 192
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<213> Homo sapiens

<400> 2

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Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg
  1               5                  10                  15

Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
             20                  25                  30

Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser
         35                  40                  45

Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
     50                  55                  60

Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp
 65                  70                  75                  80

Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn
                 85                  90                  95

Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
            100                 105                 110

Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr
        115                 120                 125
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Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
    130                 135                 140

Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly
145                 150                 155                 160

Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly
                165                 170                 175

Lys Lys Arg Arg Lys Asn Lys Lys Gln Pro Thr Phe Phe Leu Trp Gln
            180                 185                 190
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<210> 3
<211> 606
<212> DNA
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tgtccattta gctgatgcat atgtgttgta atggttttca gaattagttc tttgaagtta 180
caatcttcat tgcattcttt ctttgcatag agttttcctt ccttgttcat tgcaagatag 240
aattcacttt ccaccccttt gattgccaca attccaactg ccactgtcct gatttccatg 300
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aggcaccact gtgttcgaca gaagagtctt ctcactctta tatcccctcc ttccatgtaa 420
tcataacttc ttgtgtgtcg ctcagggctg gaacagttca catttgtagc catttgctct 480
ggagtcatgt cattgcaagc taaagatata gtacccacta gacagataat gtgaaagcat 540
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ctggtg                                                          606
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<212> PRT
<213> Homo sapiens

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Met His Lys Trp Ile Leu Thr Trp Ile Pro Pro Thr Leu Leu Tyr Arg
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Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
             20                  25                  30

Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser
         35                  40                  45

Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
     50                  55                  60

Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Cys Leu Arg Ile Asp
 65                  70                  75                  80

Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn
                 85                  90                  95

Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
            100                 105                 110
```

```
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr
        115                 120                 125

Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
    130                 135                 140

Lys Thr Ile Thr Thr His Met His Gln Leu Asn Gly His Thr Thr Glu
145                 150                 155                 160

Gly Lys Cys Leu Leu Pro
                165
```

<210> 5
<211> 582
<212> DNA
<213> Homo sapiens

<400> 5

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attatctgtc tagtgggtac tatatcttta gcttgcaatg acatgactcc agagcaaatg 120
gctacaaatg tgaactgttc cagccctgag cgacacacaa gaagttatga ttacatggaa 180
ggaggggata taagagtgag aagactcttc tgtcgaacac agtggtacct gaggatcgat 240
aaaagaggca aagtaaaagg gacccaagag atgaagaata attacaatat catggaaatc 300
aggacagtgg cagttggaat tgtggcaatc aaaggggtgg aaagtgaatt ctatcttgca 360
atgaacaagg aaggaaaact ctatgcaaag aaagaatgca atgaagattg taacttcaaa 420
gaactaattc tggaaaacca ttacaacaca tatgcatcag ctaaatggac acacaacgga 480
ggggaaatgt ttgttgcctt aaatcaaaag gggattcctg taagaggaaa aaaaacgaag 540
aaagaacaaa aaacagccca ctttcttcct atggcaataa ct                    582
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<210> 6
<211> 194
<212> PRT
<213> Homo sapiens

<400> 6

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Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg
  1               5                  10                  15

Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
             20                  25                  30

Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser
         35                  40                  45

Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
     50                  55                  60

Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp
 65                  70                  75                  80

Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn
                 85                  90                  95

Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
            100                 105                 110
```

```
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr
        115                 120                 125

Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
    130                 135                 140

Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly
145                 150                 155                 160

Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly
                165                 170                 175

Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala
            180                 185                 190

Ile Thr
```